

# SEQUENCE LISTING

<110> Yumin, Tao  
 Gordon-Kamm, William  
 Shen, Bo  
 Lowe, Keith  
 Danilevskaya, Olga  
 Mahajan, Pramod  
 Rafalski, Jan Antoni  
 Sakai, Hajime  
 Klein, Theodore

<120> Transcriptional Regulatory Nucleic  
 Acids, Polypeptides, and Methods of Use Thereof

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Arg Lys Ala Ala Ala Glu Ala Glu Asn Ser Glu Arg Asn Tyr Trp Asp	
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Glu Leu Leu Lys Asp Arg Tyr Asp Val Gln Lys Val Glu Glu His Thr	
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Glu Asp Asp Ile His Asp Leu Ser Ser Glu Asp Glu Asp Tyr Ser Leu	
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Glu Asp Asp Ile Ser Asp Asn Asp Thr Ser Leu Gln Gly Asn Ile Ser	
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Lys Tyr Phe Arg Leu Asp Gly Ser Ser Ala Ile Ser Asp Arg Arg Asp  
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Val Ile Phe Tyr Glu Ile Asp Trp Asn Pro Thr Gln Asp Gln Gln Ala  
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aag cag aaa aat gca gtg caa gag tta gtt atg aag ggg aaa cat gtc 488  
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 Lys His Val Gln Asp Asp His Leu Met Arg Gln Glu Asp Val Val Ser  
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Glu Phe Lys Thr Trp Ala Pro Ser Ile Gly Thr Ile Leu Tyr Asp Gly  
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aag ttc cta aag aaa gtt cac tgg cat tat ttg att gtt gat gaa gga 239  
Lys Phe Leu Lys Lys Val His Trp His Tyr Leu Ile Val Asp Glu Gly  
65 70 75

cat cgt ctg aaa aat cat gaa tgt gct ctt gct cgc aca cta gtt tca 287  
His Arg Leu Lys Asn His Glu Cys Ala Leu Ala Arg Thr Leu Val Ser  
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gga tat cag atc cgc cgc aga cta ctt tta act ggc act cca atc caa 335  
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1913

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35 40 45  
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50 55 60  
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65 70 75 80  
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85 90 95  
Tyr Gln Ile Arg Arg Arg Leu Leu Leu Thr Gly Thr Pro Ile Gln Asn  
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Ser Leu Gln Glu Leu Trp Ser Leu Leu Asn Phe Ile Leu Pro Asn Ile  
115 120 125  
Phe Asn Ser Ser Gln Asn Phe Glu Glu Trp Phe Asn Ala Pro Phe Ala  
130 135 140  
Cys Asp Val Ser Leu Asn Asp Glu Glu Gln Leu Leu Ile Ile His Arg  
145 150 155 160  
Leu His Gln Val Leu Arg Pro Phe Leu Leu Arg Arg Lys Lys Asp Glu  
165 170 175  
Val Glu Lys Tyr Leu Pro Val Lys Thr Gln Val Ile Leu Lys Cys Asp  
180 185 190  
Met Ser Ala Trp Gln Lys Ala Tyr Tyr Glu Gln Val Thr Ser Arg Glu  
195 200 205  
Lys Val Ala Leu Gly Phe Gly Leu Arg Ser Lys Ala Leu Gln Asn Leu  
210 215 220  
Ser Met Gln Leu Arg Lys Cys Cys Asn His Pro Tyr Leu Phe Val Glu  
225 230 235 240  
His Tyr Asn Met Tyr Gln Arg Glu Glu Ile Val Arg Ala Ser Gly Lys  
245 250 255  
Phe Glu Leu Leu Asp Arg Leu Leu Pro Lys Leu Gln Arg Ala Gly His  
260 265 270  
Arg Val Leu Leu Phe Ser Gln Met Thr Lys Leu Leu Asp Val Leu Glu  
275 280 285  
Ile Tyr Leu Gln Met Tyr Asn Phe Lys Tyr Met Arg Leu Asp Gly Ser  
290 295 300  
Thr Lys Thr Glu Glu Arg Gly Arg Leu Leu Ala Asp Phe Asn Lys Lys  
305 310 315 320  
Asp Ser Glu Tyr Phe Met Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu  
325 330 335  
Gly Leu Asn Leu Gln Thr Ala Asp Thr Val Ile Ile Phe Asp Ser Asp  
340 345 350

Trp	Asn	Pro	Gln	Met	Asp	Gln	Gln	Ala	Glu	Asp	Arg	Ala	His	Arg	Ile	
		355					360					365				
Gly	Arg	Arg	Met	Lys	Cys	Val	Cys	Leu	Phe	Leu	Leu	Val	Ser	Ala	Pro	
	370					375					380					
Leu	Lys	Lys	Arg	Ser	Trp	Thr	Val	Gln	Asn	Lys	Arg	Trp	Val	Ser	Met	
385					390					395					400	
Gln	Lys	Leu	Leu	Gln	Ala	Gly	Leu	Phe	Asn	Thr	Thr	Ser	Thr	Ala	Gln	
				405					410					415		
Asp	Arg	Arg	Ala	Leu	Leu	Gln	Glu	Ile	Leu	Arg	Arg	Gly	Thr	Ser	Ser	
			420					425					430			
Leu	Gly	Thr	Asp	Ile	Pro	Ser	Glu	Arg	Glu	Ile	Asn	Arg	Leu	Ala	Ala	
	435						440					445				
Arg	Thr	Asp	Glu	Glu	Phe	Trp	Leu	Phe	Glu	Lys	Met	Asp	Glu	Glu	Arg	
	450					455					460					
Arg	Leu	Arg	Glu	Asn	Tyr	Lys	Ser	Arg	Leu	Met	Asp	Gly	Asn	Glu	Val	
465					470					475					480	
Pro	Asp	Trp	Val	Phe	Ala	Asn	Asn	Asp	Leu	Pro	Lys	Arg	Thr	Val	Ala	
				485					490					495		
Asp	Glu	Phe	Gln	Asn	Ile	Met	Val	Gly	Ala	Lys	Arg	Arg	Arg	Lys	Glu	
			500					505					510			
Val	Val	Tyr	Ser	Asp	Ser	Phe	Gly	Asp	Gln	Trp	Met	Lys	Ser	Asp	Glu	
	515						520					525				
Gly	Phe	Glu	Asp	Ile	Pro	Lys	Ala	Thr	Gln	Arg	Ser	Lys	Lys	Thr	Ala	
	530					535					540					
Tyr	Ser	Ser	Asp	Ile	Gln	Val	Glu	Phe	Ser	Glu	Arg	Arg	Lys	Arg	Pro	
545					550					555					560	
Arg	Ser	Val	Glu	Asn	Ser	Ala	Asp	Gly	Val	Ser	Asn	Pro	Thr	Trp	Thr	
				565					570					575		
Pro	Asp	Lys	Gly	Arg	Ala	Gly	Val	Ser	Ser	Tyr	Ser	Lys	Asp	Glu	Thr	
			580					585					590			
Glu	Asp	Asp	Gly	Glu	Asp	Glu	Val	Ile	Thr	Ser	Gly	Leu	Gln	Lys	Gly	
	595						600					605				
Asn	Ser	Phe	Thr	Trp	Asn	Thr	Leu	Gly	Arg	Arg	Arg	Ser	Ser	His	Phe	
	610					615					620					
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625					630					635						

<210> 11  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <222> (1)...(23)

<400> 11  
 cgaattcaaa acctgggctc cca

23

<210> 12  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind

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<222> (1)...(21)

<400> 12
ttagaatgtt gggcgccctc t                                     21

<210> 13
<211> 1463
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (3)...(1460)

<221> misc_feature
<222> (0)...(0)
<223> n = A, T, C, or G

<400> 13
gt cga ccc acg cgt ccg cca gaa gag cgg aac cat ata agg gac aat      47
  Arg Pro Thr Arg Pro Pro Glu Glu Arg Asn His Ile Arg Asp Asn
    1             5             10             15

ttg ctg caa cct ggg aaa ttt gat gtg tgt gtg act agt ttt gaa atg      95
Leu Leu Gln Pro Gly Lys Phe Asp Val Cys Val Thr Ser Phe Glu Met
          20             25             30

gca atc aaa gaa aaa tct gcg ttg agg cgc ttc agc tgg cgc tac ata      143
Ala Ile Lys Glu Lys Ser Ala Leu Arg Arg Phe Ser Trp Arg Tyr Ile
          35             40             45

atc att gat gaa gct cac cgg ata aaa aat gaa aat tct ctt cta tca      191
Ile Ile Asp Glu Ala His Arg Ile Lys Asn Glu Asn Ser Leu Leu Ser
          50             55             60

aag act atg agg att tac aac act aat tat cgt ctc ctc atc aca ggc      239
Lys Thr Met Arg Ile Tyr Asn Thr Asn Tyr Arg Leu Leu Ile Thr Gly
          65             70             75

act cca ctc cag aat aat ctc cat gag ctc tgg gct ctc ctc aat ttc      287
Thr Pro Leu Gln Asn Asn Leu His Glu Leu Trp Ala Leu Leu Asn Phe
          80             85             90             95

ttg cta cct gaa ata ttt agc tct gcg gag acc ttt gat gaa tgg ttt      335
Leu Leu Pro Glu Ile Phe Ser Ser Ala Glu Thr Phe Asp Glu Trp Phe
          100            105            110

caa ata tct ggg gaa aat gat caa cag gag gtg gtg cag cag ctt cat      383
Gln Ile Ser Gly Glu Asn Asp Gln Gln Glu Val Val Gln Gln Leu His
          115            120            125

aag gtt ctt cgc cca ttc ctt ctt agg agg ctc aag tct gat gta naa      431
Lys Val Leu Arg Pro Phe Leu Leu Arg Arg Leu Lys Ser Asp Val Xaa
          130            135            140

aag ggc cta cct cca aag aaa gaa aca att ctt aaa gtt gga atg tct      479

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Lys	Gly	Leu	Pro	Pro	Lys	Lys	Glu	Thr	Ile	Leu	Lys	Val	Gly	Met	Ser	
145						150					155					
cag	atg	caa	aag	cag	tac	tat	cgt	gct	ctg	ctt	cag	aag	gat	ttg	gag	527
Gln	Met	Gln	Lys	Gln	Tyr	Tyr	Arg	Ala	Leu	Leu	Gln	Lys	Asp	Leu	Glu	
160					165					170					175	
ggt	att	aat	gct	ggt	ggt	gaa	cgc	aag	cga	ttg	ctt	aac	att	gcc	atg	575
Val	Ile	Asn	Ala	Gly	Gly	Glu	Arg	Lys	Arg	Leu	Leu	Asn	Ile	Ala	Met	
				180					185					190		
cag	ttg	cgc	aag	tgc	tgc	aac	cat	cca	tat	tta	ttc	caa	gga	gct	gaa	623
Gln	Leu	Arg	Lys	Cys	Cys	Asn	His	Pro	Tyr	Leu	Phe	Gln	Gly	Ala	Glu	
			195					200					205			
cct	ggg	cca	ccc	tac	aca	act	ggt	gaa	cat	cta	att	gag	aat	gca	gga	671
Pro	Gly	Pro	Pro	Tyr	Thr	Thr	Gly	Glu	His	Leu	Ile	Glu	Asn	Ala	Gly	
		210					215					220				
aaa	atg	gtt	cta	ctt	gat	aaa	ttg	ctg	ccc	aag	cta	aag	gag	cgt	gat	719
Lys	Met	Val	Leu	Leu	Asp	Lys	Leu	Leu	Pro	Lys	Leu	Lys	Glu	Arg	Asp	
	225					230					235					
tcc	aga	gtc	ctt	att	ttt	tca	cag	atg	acc	agg	ctt	ttg	gat	atc	ttg	767
Ser	Arg	Val	Leu	Ile	Phe	Ser	Gln	Met	Thr	Arg	Leu	Leu	Asp	Ile	Leu	
240					245					250					255	
gaa	gat	tat	ctt	atg	tat	agg	gga	tat	cag	tat	tgt	cga	att	gat	gga	815
Glu	Asp	Tyr	Leu	Met	Tyr	Arg	Gly	Tyr	Gln	Tyr	Cys	Arg	Ile	Asp	Gly	
				260					265					270		
aat	aca	ggt	gga	gaa	gat	cgt	gat	gca	tcc	att	gaa	gcc	ttc	aat	agt	863
Asn	Thr	Gly	Gly	Glu	Asp	Arg	Asp	Ala	Ser	Ile	Glu	Ala	Phe	Asn	Ser	
			275					280					285			
cca	gga	agt	gag	aag	ttt	gtt	ttc	tta	ctt	tca	act	agg	gca	ggt	ggc	911
Pro	Gly	Ser	Glu	Lys	Phe	Val	Phe	Leu	Leu	Ser	Thr	Arg	Ala	Gly	Gly	
		290					295					300				
ctt	ggt	atc	aac	ttg	gcc	act	gct	gat	gtt	gtg	gtt	ctc	tat	gac	agc	959
Leu	Gly	Ile	Asn	Leu	Ala	Thr	Ala	Asp	Val	Val	Val	Leu	Tyr	Asp	Ser	
	305					310					315					
gat	tgg	aat	ccc	caa	gct	gat	ctg	caa	gct	cag	gac	cgt	gca	cat	aga	1007
Asp	Trp	Asn	Pro	Gln	Ala	Asp	Leu	Gln	Ala	Gln	Asp	Arg	Ala	His	Arg	
320					325					330					335	
ata	ggt	caa	aaa	gaa	aga	agt	tca	agt	gtt	ccg	ctt	ttg	cac	ttg	agt	1055
Ile	Gly	Gln	Lys	Glu	Arg	Ser	Ser	Ser	Val	Pro	Leu	Leu	His	Leu	Ser	
				340					345					350		
tca	act	att	gag	gaa	aag	gtg	att	gag	aga	gca	tat	aag	aag	cta	gca	1103
Ser	Thr	Ile	Glu	Lys	Val	Ile	Glu	Arg	Ala	Tyr	Lys	Lys	Lys	Leu	Ala	
			355				360					365				
ttg	gat	gct	ttg	gtt	att	cag	caa	gga	cga	ttg	gca	gag	cag	aaa	act	1151

Leu Asp Ala Leu Val Ile Gln Gln Gly Arg Leu Ala Glu Gln Lys Thr	
370 375 380	
gtc aat aag gat gat ctt ctg caa atg gtg cgg ttt ggt gct gaa atg	1199
Val Asn Lys Asp Asp Leu Leu Gln Met Val Arg Phe Gly Ala Glu Met	
385 390 395	
gtt ttc agt tct aag gac agc aca ata act gat gag gac att gac cgt	1247
Val Phe Ser Ser Lys Asp Ser Thr Ile Thr Asp Glu Asp Ile Asp Arg	
400 405 410 415	
att ata gct aaa gga gag gag aca aca gca gaa ctt gat gcg aaa atg	1295
Ile Ile Ala Lys Gly Glu Glu Thr Thr Ala Glu Leu Asp Ala Lys Met	
420 425 430	
aaa aag ttc act gag gat gcc atc aaa ttt aag atg gat gat aat gct	1343
Lys Lys Phe Thr Glu Asp Ala Ile Lys Phe Lys Met Asp Asp Asn Ala	
435 440 445	
gaa ttg tat gac ttc gat gat gag aag gat gaa aac aag gtt gat ttc	1391
Glu Leu Tyr Asp Phe Asp Asp Glu Lys Asp Glu Asn Lys Val Asp Phe	
450 455 460	
aag aaa ctt gtt agt gat aac tgg att gag cca cct aga aga gaa agg	1439
Lys Lys Leu Val Ser Asp Asn Trp Ile Glu Pro Pro Arg Arg Glu Arg	
465 470 475	
aag nga aac tac tct gag tct tga	1463
Lys Xaa Asn Tyr Ser Glu Ser	
480 485	

<210> 14  
 <211> 486  
 <212> PRT  
 <213> Zea mays

<220>  
 <221> VARIANT  
 <222> (0)...(0)  
 <223> Xaa = Any Amino Acid

<400> 14

Arg Pro Thr Arg Pro Pro Glu Glu Arg Asn His Ile Arg Asp Asn Leu	
1 5 10 15	
Leu Gln Pro Gly Lys Phe Asp Val Cys Val Thr Ser Phe Glu Met Ala	
20 25 30	
Ile Lys Glu Lys Ser Ala Leu Arg Arg Phe Ser Trp Arg Tyr Ile Ile	
35 40 45	
Ile Asp Glu Ala His Arg Ile Lys Asn Glu Asn Ser Leu Leu Ser Lys	
50 55 60	
Thr Met Arg Ile Tyr Asn Thr Asn Tyr Arg Leu Ile Thr Gly Thr	
65 70 75 80	
Pro Leu Gln Asn Asn Leu His Glu Leu Trp Ala Leu Leu Asn Phe Leu	
85 90 95	
Leu Pro Glu Ile Phe Ser Ser Ala Glu Thr Phe Asp Glu Trp Phe Gln	





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<221> primer_bind
<222> (1)...(23)

<400> 15
ccagaagagc ggaaccatat aag                                     23

<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<222> (1)...(23)

<400> 16
ctcttctagg tggctcaatc cag                                     23

<210> 17
<211> 1645
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (2)...(1642)

<221> misc_feature
<222> (0)...(0)
<223> n = A, T, C, or G

<400> 17
a gca gat ggg aga aga tac atg atc cgc cgg aga cta ctt tta aca ggc      49
Ala Asp Gly Arg Arg Tyr Met Ile Arg Arg Arg Leu Leu Leu Thr Gly
  1             5             10             15

act cct atc caa aac agc ctg caa gag ctc tgg tct ttg ctt aac ttc      97
Thr Pro Ile Gln Asn Ser Leu Gln Glu Leu Trp Ser Leu Leu Asn Phe
          20             25             30

atc ctg ccc aat att ttt aat tca tcc cag aat ttt gag gaa tgg ttt      145
Ile Leu Pro Asn Ile Phe Asn Ser Ser Gln Asn Phe Glu Glu Trp Phe
          35             40             45

aat gca cca ttt gca tgt gat gtc agt ctt aat gat gag gaa caa cta      193
Asn Ala Pro Phe Ala Cys Asp Val Ser Leu Asn Asp Glu Glu Gln Leu
          50             55             60

cta atc ata cat cgt ttg cat caa gtt ttg cgt cca ttc ttg ctg agg      241
Leu Ile Ile His Arg Leu His Gln Val Leu Arg Pro Phe Leu Leu Arg
          65             70             75             80

agg aag aaa gat gaa gta nag aaa tat ctc cct gtg aaa aca caa gta      289
Arg Lys Lys Asp Glu Val Xaa Lys Tyr Leu Pro Val Lys Thr Gln Val
          85             90             95

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att ctc aag tgt gac atg tct gct tgg caa aaa gca tac tac gaa caa Ile Leu Lys Cys Asp Met Ser Ala Trp Gln Lys Ala Tyr Tyr Glu Gln 100 105 110	337
gtc aca agc agg gaa aag gtt gcg cta gga tat ggg atc aga aag aag Val Thr Ser Arg Glu Lys Val Ala Leu Gly Tyr Gly Ile Arg Lys Lys 115 120 125	385
gct ctg caa aat ctg tca atg caa ctt agg aag tgt tgc aat cat ccc Ala Leu Gln Asn Leu Ser Met Gln Leu Arg Lys Cys Cys Asn His Pro 130 135 140	433
tac cta ttc gta gag cat tat aac atg tac caa cgg gag gaa ata gtt Tyr Leu Phe Val Glu His Tyr Asn Met Tyr Gln Arg Glu Glu Ile Val 145 150 155 160	481
aga gca tcc gga aag ttt gaa ttg ctt gat cgt cta ctt ccg aaa ttg Arg Ala Ser Gly Lys Phe Glu Leu Leu Asp Arg Leu Leu Pro Lys Leu 165 170 175	529
cag aga gct ggt cac agg gtt tta ctt ttc tct cag atg aca aaa ttg Gln Arg Ala Gly His Arg Val Leu Leu Phe Ser Gln Met Thr Lys Leu 180 185 190	577
ctt gac gtt tta gaa ata tat ttg cag atg tac aat ttc aag tac atg Leu Asp Val Leu Glu Ile Tyr Leu Gln Met Tyr Asn Phe Lys Tyr Met 195 200 205	625
agg ctt gat gga tcc aca aag act gaa gaa cgt ggg agg tta ctg gca Arg Leu Asp Gly Ser Thr Lys Thr Glu Glu Arg Gly Arg Leu Leu Ala 210 215 220	673
gat ttt aat aag aag aat tca gaa tat ttc atg ttt ctt ctc agc aca Asp Phe Asn Lys Lys Asn Ser Glu Tyr Phe Met Phe Leu Leu Ser Thr 225 230 235 240	721
cga gcc gga ggt ctt gga ttg aac ttg cag act gca gac acc gtc att Arg Ala Gly Gly Leu Gly Leu Asn Leu Gln Thr Ala Asp Thr Val Ile 245 250 255	769
atc ttt gat agt gac tgg aac cct cag atg gac caa caa gct gag gac Ile Phe Asp Ser Asp Trp Asn Pro Gln Met Asp Gln Gln Ala Glu Asp 260 265 270	817
cgt gcc cat cgt ata ggg caa aag aac gaa gta cgt gtg ttt gtt ctt Arg Ala His Arg Ile Gly Gln Lys Asn Glu Val Arg Val Phe Val Leu 275 280 285	865
gtt agc gtt ggt tca att gaa gaa gag ata ttg gat cgt gcg aaa cag Val Ser Val Gly Ser Ile Glu Glu Glu Ile Leu Asp Arg Ala Lys Gln 290 295 300	913
aag atg ggt att gat gca aaa gta atc cag gct ggg ttg ttt aac acg Lys Met Gly Ile Asp Ala Lys Val Ile Gln Ala Gly Leu Phe Asn Thr 305 310 315 320	961

acc tcc aca gca cag gac agg cga gca ttg ctg cag gag ata ctc agg	1009
Thr Ser Thr Ala Gln Asp Arg Arg Ala Leu Leu Gln Glu Ile Leu Arg	
325 330 335	
aga gga aca agc tca ctg gga acg gat atc ccc agt gaa cgt gag ata	1057
Arg Gly Thr Ser Ser Leu Gly Thr Asp Ile Pro Ser Glu Arg Glu Ile	
340 345 350	
aac cgc ttg gct gct cga aac gat gaa gaa ttc cgg ttg ttt gag aag	1105
Asn Arg Leu Ala Ala Arg Asn Asp Glu Glu Phe Arg Leu Phe Glu Lys	
355 360 365	
atg gat gaa gaa agg agg cta aag gag aac tac aaa tct aga ctt atg	1153
Met Asp Glu Glu Arg Arg Leu Lys Glu Asn Tyr Lys Ser Arg Leu Met	
370 375 380	
gat gga aat gag gtc cca gat tgg gtg ttt gcc aat gat aat gaa acc	1201
Asp Gly Asn Glu Val Pro Asp Trp Val Phe Ala Asn Asp Asn Glu Thr	
385 390 395 400	
tta cgc aag aaa acc gtg gca gat gaa ttc cgg aat ata att gtt ggt	1249
Leu Arg Lys Lys Thr Val Ala Asp Glu Phe Arg Asn Ile Ile Val Gly	
405 410 415	
tca aag aga cgt aga aag gag gtt gtc tat tcg gac tct ttt ggt gat	1297
Ser Lys Arg Arg Arg Lys Glu Val Val Tyr Ser Asp Ser Phe Gly Asp	
420 425 430	
cag tgg atg aaa tcc gac gag gga ttt gaa gag att gca aag atg act	1345
Gln Trp Met Lys Ser Asp Glu Gly Phe Glu Glu Ile Ala Lys Met Thr	
435 440 445	
cca agg gtg aag cga act gct tat tcg cct gac att caa gtt gag tac	1393
Pro Arg Val Lys Arg Thr Ala Tyr Ser Pro Asp Ile Gln Val Glu Tyr	
450 455 460	
aat gaa agg agg aaa agg ccc aag tct gtg gaa aac agc gca gat ggc	1441
Asn Glu Arg Arg Lys Arg Pro Lys Ser Val Glu Asn Ser Ala Asp Gly	
465 470 475 480	
gca agc aac cca aca cgg aca ccc gac aaa gga agg gct gga gtt tca	1489
Ala Ser Asn Pro Thr Arg Thr Pro Asp Lys Gly Arg Ala Gly Val Ser	
485 490 495	
tca tac agc aag gat gag acc gaa gat gat ggt gaa gac gaa gtc atc	1537
Ser Tyr Ser Lys Asp Glu Thr Glu Asp Asp Gly Glu Asp Glu Val Ile	
500 505 510	
acc agt ggc tta cag aag ggt aac agt ttc aca tgg aag acc ctt gga	1585
Thr Ser Gly Leu Gln Lys Gly Asn Ser Phe Thr Trp Lys Thr Leu Gly	
515 520 525	
aga aaa agg tca agc cac tta agt tcg tcg tcg gac tca aaa ggg cga	1633
Arg Lys Arg Ser Ser His Leu Ser Ser Ser Ser Asp Ser Lys Gly Arg	
530 535 540	

cca tca ttc taa  
Pro Ser Phe  
545

1645

<210> 18  
<211> 547  
<212> PRT  
<213> Zea mays

<220>  
<221> VARIANT  
<222> (0)...(0)  
<223> Xaa = any amino acid

<400> 18  
Ala Asp Gly Arg Arg Tyr Met Ile Arg Arg Arg Leu Leu Leu Thr Gly  
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Thr Pro Ile Gln Asn Ser Leu Gln Glu Leu Trp Ser Leu Leu Asn Phe  
20 25 30  
Ile Leu Pro Asn Ile Phe Asn Ser Ser Gln Asn Phe Glu Glu Trp Phe  
35 40 45  
Asn Ala Pro Phe Ala Cys Asp Val Ser Leu Asn Asp Glu Glu Gln Leu  
50 55 60  
Leu Ile Ile His Arg Leu His Gln Val Leu Arg Pro Phe Leu Leu Arg  
65 70 75 80  
Arg Lys Lys Asp Glu Val Xaa Lys Tyr Leu Pro Val Lys Thr Gln Val  
85 90 95  
Ile Leu Lys Cys Asp Met Ser Ala Trp Gln Lys Ala Tyr Tyr Glu Gln  
100 105 110  
Val Thr Ser Arg Glu Lys Val Ala Leu Gly Tyr Gly Ile Arg Lys Lys  
115 120 125  
Ala Leu Gln Asn Leu Ser Met Gln Leu Arg Lys Cys Cys Asn His Pro  
130 135 140  
Tyr Leu Phe Val Glu His Tyr Asn Met Tyr Gln Arg Glu Glu Ile Val  
145 150 155 160  
Arg Ala Ser Gly Lys Phe Glu Leu Leu Asp Arg Leu Leu Pro Lys Leu  
165 170 175  
Gln Arg Ala Gly His Arg Val Leu Leu Phe Ser Gln Met Thr Lys Leu  
180 185 190  
Leu Asp Val Leu Glu Ile Tyr Leu Gln Met Tyr Asn Phe Lys Tyr Met  
195 200 205  
Arg Leu Asp Gly Ser Thr Lys Thr Glu Glu Arg Gly Arg Leu Leu Ala  
210 215 220  
Asp Phe Asn Lys Lys Asn Ser Glu Tyr Phe Met Phe Leu Leu Ser Thr  
225 230 235 240  
Arg Ala Gly Gly Leu Gly Leu Asn Leu Gln Thr Ala Asp Thr Val Ile  
245 250 255  
Ile Phe Asp Ser Asp Trp Asn Pro Gln Met Asp Gln Gln Ala Glu Asp  
260 265 270  
Arg Ala His Arg Ile Gly Gln Lys Asn Glu Val Arg Val Phe Val Leu  
275 280 285  
Val Ser Val Gly Ser Ile Glu Glu Glu Ile Leu Asp Arg Ala Lys Gln  
290 295 300  
Lys Met Gly Ile Asp Ala Lys Val Ile Gln Ala Gly Leu Phe Asn Thr  
305 310 315 320

Thr Ser Thr Ala Gln Asp Arg Arg Ala Leu Leu Gln Glu Ile Leu Arg  
 325 330 335  
 Arg Gly Thr Ser Ser Leu Gly Thr Asp Ile Pro Ser Glu Arg Glu Ile  
 340 345 350  
 Asn Arg Leu Ala Ala Arg Asn Asp Glu Glu Phe Arg Leu Phe Glu Lys  
 355 360 365  
 Met Asp Glu Glu Arg Arg Leu Lys Glu Asn Tyr Lys Ser Arg Leu Met  
 370 375 380  
 Asp Gly Asn Glu Val Pro Asp Trp Val Phe Ala Asn Asp Asn Glu Thr  
 385 390 395 400  
 Leu Arg Lys Lys Thr Val Ala Asp Glu Phe Arg Asn Ile Ile Val Gly  
 405 410 415  
 Ser Lys Arg Arg Arg Lys Glu Val Val Tyr Ser Asp Ser Phe Gly Asp  
 420 425 430  
 Gln Trp Met Lys Ser Asp Glu Gly Phe Glu Glu Ile Ala Lys Met Thr  
 435 440 445  
 Pro Arg Val Lys Arg Thr Ala Tyr Ser Pro Asp Ile Gln Val Glu Tyr  
 450 455 460  
 Asn Glu Arg Arg Lys Arg Pro Lys Ser Val Glu Asn Ser Ala Asp Gly  
 465 470 475 480  
 Ala Ser Asn Pro Thr Arg Thr Pro Asp Lys Gly Arg Ala Gly Val Ser  
 485 490 495  
 Ser Tyr Ser Lys Asp Glu Thr Glu Asp Asp Gly Glu Asp Glu Val Ile  
 500 505 510  
 Thr Ser Gly Leu Gln Lys Gly Asn Ser Phe Thr Trp Lys Thr Leu Gly  
 515 520 525  
 Arg Lys Arg Ser Ser His Leu Ser Ser Ser Ser Asp Ser Lys Gly Arg  
 530 535 540  
 Pro Ser Phe  
 545

<210> 19  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <222> (1)...(23)

<400> 19  
 acaggcactc ctatccaaaa cag

23

<210> 20  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <222> (1)...(23)

<400> 20  
 gaatgatggt cgcccttttg agt

23

<210> 21

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<211> 514
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (6)...(514)

<221> misc_feature
<222> (0)...(0)
<223> n = A, T, C, or G

<400> 21
ccnta aat ttc ttg tta ccc aaa cnt nat caa ttt cat cca gga gga ctt      50
      Asn Phe Leu Leu Pro Lys Xaa Xaa Gln Phe His Pro Gly Gly Leu
        1             5             10             15

ctc tca aat ggt tta ata agc cat ttg aga gtg ctt gga gat agc tcg      98
Leu Ser Asn Gly Leu Ile Ser His Leu Arg Val Leu Gly Asp Ser Ser
          20             25             30

cct gat gaa gct tta ntg tcc gag gag gag aat ctc ttg att ata aat      146
Pro Asp Glu Ala Leu Xaa Ser Glu Glu Glu Asn Leu Leu Ile Ile Asn
          35             40             45

cgt ctg cac caa gtt ttg aga cca ttt gta ctt agg agg ctg aaa cac      194
Arg Leu His Gln Val Leu Arg Pro Phe Val Leu Arg Arg Leu Lys His
          50             55             60

aag gtt gaa aat gag ttg cct gag aag att gag aga cta ata aga tgt      242
Lys Val Glu Asn Glu Leu Pro Glu Lys Ile Glu Arg Leu Ile Arg Cys
          65             70             75

gag gcc tca tca tat caa aaa ctt ttg atg aag agg gtg gaa gaa aat      290
Glu Ala Ser Ser Tyr Gln Lys Leu Leu Met Lys Arg Val Glu Glu Asn
          80             85             90             95

ctt ggt tct att ggc aat tca aag gct cga tca gta cac aac tct gtc      338
Leu Gly Ser Ile Gly Asn Ser Lys Ala Arg Ser Val His Asn Ser Val
          100            105            110

atg gag ctt cgt aat ata tgc aat cat cca tat ctc agt cag ctt cat      386
Met Glu Leu Arg Asn Ile Cys Asn His Pro Tyr Leu Ser Gln Leu His
          115            120            125

gca gag gag gtg gat aac ttc ata cct aaa cat tat ctg cca cca att      434
Ala Glu Glu Val Asp Asn Phe Ile Pro Lys His Tyr Leu Pro Pro Ile
          130            135            140

att aga ctt tgt ggg aag ctt gag atg ttg gac cgt tta ttg cca aaa      482
Ile Arg Leu Cys Gly Lys Leu Glu Met Leu Asp Arg Leu Leu Pro Lys
          145            150            155

ttg aag gcg aca gat cat cgg gtt ctt ttc tt      514
Leu Lys Ala Thr Asp His Arg Val Leu Phe
160             165

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<210> 22  
 <211> 169  
 <212> PRT  
 <213> Glycine max

<220>  
 <221> VARIANT  
 <222> (0)...(0)  
 <223> Xaa = Any Amino Acid

<400> 22  
 Asn Phe Leu Leu Pro Lys Xaa Xaa Gln Phe His Pro Gly Gly Leu Leu  
 1 5 10 15  
 Ser Asn Gly Leu Ile Ser His Leu Arg Val Leu Gly Asp Ser Ser Pro  
 20 25 30  
 Asp Glu Ala Leu Xaa Ser Glu Glu Asn Leu Leu Ile Ile Asn Arg  
 35 40 45  
 Leu His Gln Val Leu Arg Pro Phe Val Leu Arg Arg Leu Lys His Lys  
 50 55 60  
 Val Glu Asn Glu Leu Pro Glu Lys Ile Glu Arg Leu Ile Arg Cys Glu  
 65 70 75 80  
 Ala Ser Ser Tyr Gln Lys Leu Leu Met Lys Arg Val Glu Glu Asn Leu  
 85 90 95  
 Gly Ser Ile Gly Asn Ser Lys Ala Arg Ser Val His Asn Ser Val Met  
 100 105 110  
 Glu Leu Arg Asn Ile Cys Asn His Pro Tyr Leu Ser Gln Leu His Ala  
 115 120 125  
 Glu Glu Val Asp Asn Phe Ile Pro Lys His Tyr Leu Pro Pro Ile Ile  
 130 135 140  
 Arg Leu Cys Gly Lys Leu Glu Met Leu Asp Arg Leu Leu Pro Lys Leu  
 145 150 155 160  
 Lys Ala Thr Asp His Arg Val Leu Phe  
 165

<210> 23  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <222> (1)...(23)

<400> 23  
 aacccgatga tctgtcgcct tca

23

<210> 24  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <222> (1)...(23)



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<400> 24
tcatccagga ggacttctct caa
23

<210> 25
<211> 403
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (221)...(403)

<221> misc_feature
<222> (0)...(0)
<223> n = A, T, C, or G

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cnaatgaatca agtgattgnt attttatttc atgtgtcacc cagccatatt ggcagatgaa 120
atgggtcttg gcaaaacagt tcagggtacgt attctgtttt ttattatttt aatatgtttc 180
ntaatttggt tgnnttccta atcctttact tttcaagtaa gaa atg cca tat gtt 235
                                Glu Met Pro Tyr Val
                                1 5

ctt gtc ttc cag gcc atc aca tat tta act ttg ctg aaa cac ttg cac 283
Leu Val Phe Gln Ala Ile Thr Tyr Leu Thr Leu Leu Lys His Leu His
                                10 15 20

aat gat tct ggt cca cat ctt ata gta tgt cct gct tct gtt ctg gaa 331
Asn Asp Ser Gly Pro His Leu Ile Val Cys Pro Ala Ser Val Leu Glu
                                25 30 35

aac tgg gaa agg gaa tta aaa agg tgg tgt cca tcc ttt tct gtt ctt 379
Asn Trp Gln Arg Glu Leu Lys Arg Trp Cys Pro Ser Phe Ser Val Leu
                                40 45 50

caa tac cat ggg gcc gga cgt gca 403
Gln Tyr His Gly Ala Gly Arg Ala
                                55 60

<210> 26
<211> 61
<212> PRT
<213> Glycine max

<220>
<221> VARIANT
<222> (0)...(0)
<223> Xaa = Any Amino Acid

<400> 26
Glu Met Pro Tyr Val Leu Val Phe Gln Ala Ile Thr Tyr Leu Thr Leu
1 5 10 15
Leu Lys His Leu His Asn Asp Ser Gly Pro His Leu Ile Val Cys Pro

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	20		25		30										
Ala	Ser	Val	Leu	Glu	Asn	Trp	Glu	Arg	Glu	Leu	Lys	Arg	Trp	Cys	Pro
	35		40		45										
Ser	Phe	Ser	Val	Leu	Gln	Tyr	His	Gly	Ala	Gly	Arg	Ala			
50			55		60										

<210> 27  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <222> (1)...(23)

<400> 27  
 gccccatggt attgaagaac aga 23

<210> 28  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <222> (1)...(25)

<400> 28  
 attttatttc atgtgtcacc cagcc 25

<210> 29  
 <211> 522  
 <212> DNA  
 <213> Oryza sativa

<220>  
 <221> CDS  
 <222> (1)...(522)

<221> misc\_feature  
 <222> (0)...(0)  
 <223> n = A, T, C or G

<400> 29  
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 Val Ser Gly Arg Lys Ala Gln Tyr Ser Lys Lys Asn Ser Arg Asn Val  
 1 5 10 15

gat tca ctc cct ttg atg gag ggt gaa ggg cgt gct tta aaa gtt tat 96  
 Asp Ser Leu Pro Leu Met Glu Gly Glu Gly Arg Ala Leu Lys Val Tyr  
 20 25 30

gga ttc aat cac gtt caa cga aca caa ttc cta cag aca ctc atg agg 144  
 Gly Phe Asn His Val Gln Arg Thr Gln Phe Leu Gln Thr Leu Met Arg  
 35 40 45

tat ggt ttt cag aac tat gat tgg aaa gag tat ctt cct cgt ttg aag	192
Tyr Gly Phe Gln Asn Tyr Asp Trp Lys Glu Tyr Leu Pro Arg Leu Lys	
50 55 60	
ggg aaa agt gtt gag gaa att cag aga tat ggt gag ctt gtc atg gcc	240
Gly Lys Ser Val Glu Glu Ile Gln Arg Tyr Gly Glu Leu Val Met Ala	
65 70 75 80	
cat ctt gta gag gac aca aat gac tca cca acc tat gca gat ggt gtg	288
His Leu Val Glu Asp Thr Asn Asp Ser Pro Thr Tyr Ala Asp Gly Val	
85 90 95	
ccg aag aaa tgc gtg ctg atg aga cat tgg tca ggc tag cca aaa tat	336
Pro Lys Lys Cys Val Leu Met Arg His Trp Ser Gly * Pro Lys Tyr	
100 105 110	
cac ttg tgg agg aga agg tgg tgc atg gag caa gga aaa tta caa aac	384
His Leu Trp Arg Arg Arg Trp Cys Met Glu Gln Gly Lys Leu Gln Asn	
115 120 125	
tct tcc cca act act tga tgt atg aat tta ctg gct tat cag gtg gaa	432
Ser Ser Pro Thr Thr * Cys Met Asn Leu Leu Ala Tyr Gln Val Glu	
130 135 140	
gaa tat gga aag ggg aac atg atc tac tgt nac tga agc ata ata agc	480
Glu Tyr Gly Lys Gly Asn Met Ile Tyr Cys Xaa * Ser Ile Ile Ser	
145 150 155	
acg ggt tgc cag tgg cat aca tat cag atn cag aga tac ggg	522
Thr Gly Cys Gln Trp His Thr Tyr Gln Xaa Gln Arg Tyr Gly	
160 165 170	

<210> 30

<211> 171

<212> PRT

<213> Oryza sativa

<220>

<221> VARIANT

<222> (0)...(0)

<223> Xaa = Any Amino Acid

<400> 30

Val Ser Gly Arg Lys Ala Gln Tyr Ser Lys Lys Asn Ser Arg Asn Val	
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Asp Ser Leu Pro Leu Met Glu Gly Glu Gly Arg Ala Leu Lys Val Tyr	
20 25 30	
Gly Phe Asn His Val Gln Arg Thr Gln Phe Leu Gln Thr Leu Met Arg	
35 40 45	
Tyr Gly Phe Gln Asn Tyr Asp Trp Lys Glu Tyr Leu Pro Arg Leu Lys	
50 55 60	
Gly Lys Ser Val Glu Glu Ile Gln Arg Tyr Gly Glu Leu Val Met Ala	
65 70 75 80	
His Leu Val Glu Asp Thr Asn Asp Ser Pro Thr Tyr Ala Asp Gly Val	
85 90 95	

Pro Lys Lys Cys Val Leu Met Arg His Trp Ser Gly Pro Lys Tyr His  
100 105 110  
Leu Trp Arg Arg Arg Trp Cys Met Glu Gln Gly Lys Leu Gln Asn Ser  
115 120 125  
Ser Pro Thr Thr Cys Met Asn Leu Leu Ala Tyr Gln Val Glu Glu Tyr  
130 135 140  
Gly Lys Gly Asn Met Ile Tyr Cys Xaa Ser Ile Ile Ser Thr Gly Cys  
145 150 155 160  
Gln Trp His Thr Tyr Gln Xaa Gln Arg Tyr Gly  
165 170

<210> 31  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> primer\_bind  
<222> (1)...(23)

<400> 31  
gtttctggga ggaaggctca gta 23

<210> 32  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> primer\_bind  
<222> (1)...(23)

<400> 32  
tatgtatgcc actggcaacc cgt 23

<210> 33  
<211> 510  
<212> DNA  
<213> Oryza sativa

<220>  
<221> CDS  
<222> (2)...(510)

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Leu Gln Asp Phe Gly Gly Gly Gly Cys Gly Cys Leu Glu Arg Arg Gly  
1 5 10 15

tta ata gct aca gca tgt gac gtt gat act cta atg atg aag gag cgg 97  
Leu Ile Ala Thr Ala Cys Asp Val Asp Thr Leu Met Met Lys Glu Arg  
20 25 30

agc tct tta tgt gaa agt gcg gca gat gga agt tgg gtt ttg aaa tac 145  
Ser Ser Leu Cys Glu Ser Ala Ala Asp Gly Ser Trp Val Leu Lys Tyr  
35 40 45

aaa agg aaa cgg agc aag cta aca gtt agt cca tca agt gag cat gat	193
Lys Arg Lys Arg Ser Lys Leu Thr Val Ser Pro Ser Ser Glu His Asp	
50 55 60	
gct tcc tca cca ata ctg gat tct caa atg aac aat ggc tcc atc aaa	241
Ala Ser Ser Pro Ile Leu Asp Ser Gln Met Asn Asn Gly Ser Ile Lys	
65 70 75 80	
aag aag atc aaa cat gac act aac att tct cca tca acc aag aag ata	289
Lys Lys Ile Lys His Asp Thr Asn Ile Ser Pro Ser Thr Lys Lys Ile	
85 90 95	
aga gga cat gac ggg tac ttc tac gag tgt gta gaa tgt gat ctc ggt	337
Arg Gly His Asp Gly Tyr Phe Tyr Glu Cys Val Glu Cys Asp Leu Gly	
100 105 110	
ggc aat ttg ctg tgc tgt gat agc tgt cca cga aca tac cac ttg gaa	385
Gly Asn Leu Leu Cys Cys Asp Ser Cys Pro Arg Thr Tyr His Leu Glu	
115 120 125	
tgt ctt aat cct cct ctc aag cgt gca cca cct gga aat tgg caa tgc	433
Cys Leu Asn Pro Pro Leu Lys Arg Ala Pro Pro Gly Asn Trp Gln Cys	
130 135 140	
cca aga tgt cgt aca aaa aaa gtt agc ttg aag ctc tta aac aat gct	481
Pro Arg Cys Arg Thr Lys Lys Val Ser Leu Lys Leu Leu Asn Asn Ala	
145 150 155 160	
gat gct gac acc tcc taa acg tga aag aa	510
Asp Ala Asp Thr Ser * Thr * Lys	
165	

<210> 34

<211> 167

<212> PRT

<213> Oryza sativa

<400> 34

Leu Gln Asp Phe Gly Gly Gly Gly Cys Gly Cys Leu Glu Arg Arg Gly	
1 5 10 15	
Leu Ile Ala Thr Ala Cys Asp Val Asp Thr Leu Met Met Lys Glu Arg	
20 25 30	
Ser Ser Leu Cys Glu Ser Ala Ala Asp Gly Ser Trp Val Leu Lys Tyr	
35 40 45	
Lys Arg Lys Arg Ser Lys Leu Thr Val Ser Pro Ser Ser Glu His Asp	
50 55 60	
Ala Ser Ser Pro Ile Leu Asp Ser Gln Met Asn Asn Gly Ser Ile Lys	
65 70 75 80	
Lys Lys Ile Lys His Asp Thr Asn Ile Ser Pro Ser Thr Lys Lys Ile	
85 90 95	
Arg Gly His Asp Gly Tyr Phe Tyr Glu Cys Val Glu Cys Asp Leu Gly	
100 105 110	
Gly Asn Leu Leu Cys Cys Asp Ser Cys Pro Arg Thr Tyr His Leu Glu	
115 120 125	

Cys Leu Asn Pro Pro Leu Lys Arg Ala Pro Pro Gly Asn Trp Gln Cys  
 130 135 140  
 Pro Arg Cys Arg Thr Lys Lys Val Ser Leu Lys Leu Leu Asn Asn Ala  
 145 150 155 160  
 Asp Ala Asp Thr Ser Thr Lys  
 165

<210> 35  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 35  
 cttacaggat ttcgggggag gtg 23

<210> 36  
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<220>  
 <221> primer\_bind  
 <222> (1)...(23)

<400> 36  
 ctttcacggt taggaggtgt cag 23

<210> 37  
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 <212> DNA  
 <213> Triticum aestivum

<220>  
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<221> misc\_feature  
 <222> (0)...(0)  
 <223> n = A, T, C, or G

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 1 5 10 15

ttg aac ttc cta cag cct gct tct ttc cct tct cta gca tca ttt gag 97  
 Leu Asn Phe Leu Gln Pro Ala Ser Phe Pro Ser Leu Ala Ser Phe Glu  
 20 25 30

gag aag ttt aat gaa ctt gca aca gca gag aaa gtg gag gag ctg aag 145  
 Glu Lys Phe Asn Glu Leu Ala Thr Ala Glu Lys Val Glu Glu Leu Lys  
 35 40 45

aaa ctg gta gca cca cat atg ctt cga agg ctg aaa aaa gat gca atg	193
Lys Leu Val Ala Pro His Met Leu Arg Arg Leu Lys Lys Asp Ala Met	
50 55 60	
aaa aat atc ccc ccg aag aca gag cga atg gtg cct gtc gaa ctg aca	241
Lys Asn Ile Pro Pro Lys Thr Glu Arg Met Val Pro Val Glu Leu Thr	
65 70 75 80	
tca atc cag gct gaa tac tac cgt gct atg ctt aca aag aac tac caa	289
Ser Ile Gln Ala Glu Tyr Tyr Arg Ala Met Leu Thr Lys Asn Tyr Gln	
85 90 95	
gta ctg cgt aat acc gga aaa ggt ggt gct cat cag tca ttg ctc aat	337
Val Leu Arg Asn Thr Gly Lys Gly Gly Ala His Gln Ser Leu Leu Asn	
100 105 110	
ata gta atg cag ctt cgg aaa ttt gca acc atc cat atc tta tcc tgg	385
Ile Val Met Gln Leu Arg Lys Phe Ala Thr Ile His Ile Leu Ser Trp	
115 120 125	
gaa ctg aac ccg aat caa gtt cac cag att ttt gca tga aat gag aat	433
Glu Leu Asn Pro Asn Gln Val His Gln Ile Phe Ala * Asn Glu Asn	
130 135 140	
aaa ggc tca aca aat taa ctt tgt tgc att cta tgc tca aag tgt tac	481
Lys Gly Ser Thr Asn * Leu Cys Cys Ile Leu Cys Ser Lys Cys Tyr	
145 150 155	
aca gtg atg ggc atc gtg ttc taa ttt tcc aga tga cta aac tct tga	529
Thr Val Met Gly Ile Val Phe * Phe Ser Arg * Leu Asn Ser *	
160 165 170	
cat ccc gaa gat anc gac ccg gaa ttg gca taa aca ntn aaa gag naa	577
His Pro Glu Asp Xaa Asp Pro Glu Leu Ala * Thr Xaa Lys Glu Xaa	
175 180 185	
tgg tcg tgt cgt ggg tga cnc aag cac ata nct tca aca gaa ana cgt	625
Trp Ser Cys Arg Gly * Xaa Lys His Ile Xaa Ser Thr Glu Xaa Arg	
190 195 200	
ttg att tgt aca acg gca tgc ntg tat tga cna nac gta can	667
Leu Ile Cys Thr Thr Ala Cys Xaa Tyr * Xaa Xaa Val Xaa	
205 210	

<210> 38  
 <211> 214  
 <212> PRT  
 <213> Triticum aestivum

<220>  
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 <222> (0)...(0)  
 <223> Xaa = Any Amino Acid

<400> 38  
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 20 25 30  
 Glu Lys Phe Asn Glu Leu Ala Thr Ala Glu Lys Val Glu Glu Leu Lys  
 35 40 45  
 Lys Leu Val Ala Pro His Met Leu Arg Arg Leu Lys Lys Asp Ala Met  
 50 55 60  
 Lys Asn Ile Pro Pro Lys Thr Glu Arg Met Val Pro Val Glu Leu Thr  
 65 70 75 80  
 Ser Ile Gln Ala Glu Tyr Tyr Arg Ala Met Leu Thr Lys Asn Tyr Gln  
 85 90 95  
 Val Leu Arg Asn Thr Gly Lys Gly Gly Ala His Gln Ser Leu Leu Asn  
 100 105 110  
 Ile Val Met Gln Leu Arg Lys Phe Ala Thr Ile His Ile Leu Ser Trp  
 115 120 125  
 Glu Leu Asn Pro Asn Gln Val His Gln Ile Phe Ala Asn Glu Asn Lys  
 130 135 140  
 Gly Ser Thr Asn Leu Cys Cys Ile Leu Cys Ser Lys Cys Tyr Thr Val  
 145 150 155 160  
 Met Gly Ile Val Phe Phe Ser Arg Leu Asn Ser His Pro Glu Asp Xaa  
 165 170 175  
 Asp Pro Glu Leu Ala Thr Xaa Lys Glu Xaa Trp Ser Cys Arg Gly Xaa  
 180 185 190  
 Lys His Ile Xaa Ser Thr Glu Xaa Arg Leu Ile Cys Thr Thr Ala Cys  
 195 200 205  
 Xaa Tyr Xaa Xaa Val Xaa  
 210

<210> 39  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <222> (1)...(23)

<400> 39  
 gttgactgga accccattac aga

23

<210> 40  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <222> (1)...(23)

<400> 40  
 catgccgttg tacaaatcaa acg

23

<210> 41  
 <211> 12561



<212> DNA

<213> Zea mays

<220>

<221> misc\_feature

<222> (1)...(12561)

<223> Zmpk1 genomic sequence

<221> misc\_feature

<222> (0)...(0)

<223> n = A, T, C, or G

<400> 41

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atggattcgc	ttcaatttct	cacctatgta	tgtacagtga	ttggaaccca	catgcggatt	120
tgcaagctat	ggcaagagct	catcgcttag	gacagactag	taaggatttt	taccttacac	180
tttatattgt	ataaaaaaac	agattttcaa	taagttttgt	ggtgatttta	taattttcat	240
ctgtttttct	tttaggtgat	gatatacagg	cttgtaggcc	gaggtacaat	tgaggagcga	300
atgatgcaga	ttacaaaaaa	gaagatttta	ttggagcact	tagttgttgg	tcgactcacc	360
aaagctaata	atgtcaatca	ggtatgttga	ctacttttta	atgggtgaatt	ttgtaaacca	420
tcaacttagg	ttgatctttt	atggcctaag	ctattttatga	attcattttat	ggattgaggg	480
ttgagtagtt	acatgttact	ccctccattt	tttatatttg	tggtgtttta	gttcaaaaat	540
aaactaacgg	gtgacaaata	ttcgagaacg	gaggtagtac	tagtaccttc	tgtctgggat	600
gacatgaaat	gaatgtagca	tctgttagta	tcatgtccat	ttcttttgtgt	tacattttac	660
aaggcttaaa	accttacaca	tattgccgga	gttggtgact	atttagtctt	atctgtaaat	720
ttagttgttt	ctcttgatgt	caatagcaat	ttatggttgt	atgagatttc	gtgggtttgt	780
tagcatgtgt	gccatatagg	tttagctccg	ctgatgtgtt	atgcacttat	aattcagacc	840
cattttgagg	ctgtgatgtg	atacacaatg	ctagttgtta	aggccccatt	tgtttgtttc	900
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cagattaata	attaacccaa	tttgctcttc	tgacctgcta	gtgagccctt	cattggtttt	1440
taagtactaa	ataataaata	tgtgtctttg	cctatttttag	gaggagttag	atgatattat	1500
acgctatgga	tcaaaggagc	tttttgaaga	cgagaatgat	gaatctcgcc	aaattcatta	1560
tgacgaagct	gcaattgaga	ggtaaacacc	taggcccttt	tttgatctcc	taagataaga	1620
ttaatgagaa	cgacgtagaa	aaatgagtgt	gatccaagca	cagattctag	aatccaacta	1680
tctagctaaa	ccttgctata	catagattct	cgctatgcaa	aggccataat	cactatgaaa	1740
atgagatcca	aacacccctt	gtttttat	atctagaatg	tagattctca	aaagaagggc	1800
aagcttggtg	cattgggtgag	atctttctca	ttcagtcatc	aagtcgtggg	ttcaaagcag	1860
cctctcgaca	tttgtgggag	cctctagcac	tgggtctacc	cctttttatt	aacaatctag	1920
attctacatc	atcatgtaga	atcactatga	taatgagatc	taaacatggc	cttaagcccc	1980
taacttcacc	ttgggaagtt	atctcgtgca	ttaagcatgc	ctttttgggtg	tgaagttgtt	2040
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gatcatggat	gcaaatctag	aattctagag	ataattagta	tgtatgccct	accaagtagg	2160
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agagttatgc	ctattagtga	gaagcttttc	ataggagatc	tcaacggaca	tgtaggtaca	2280
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catgtagtag	tggaacacgc	tctagtcaga	tttgtaaagt	aactgtgtat	tccttgtaat	2400
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<400> 43

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Val	Leu	Glu	Ala	Pro	Arg	Glu	Asp	Ser	Ser	Ser	Thr	Glu	Pro	Arg	Ser

Lys	Lys	Met	Glu	Arg	Tyr	Leu	Ile	Lys	Trp	Lys	Gly	Leu	Ser	Tyr	Ile
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His	Pro	Arg	Leu	Arg	Thr	Arg	Leu	Asn	Asn	Phe	Arg	Arg	Gln	Lys	Glu
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Asn															

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Asp	Lys	Met	Met	Val	Lys	Leu	Lys	Glu	Gln	Gly	His	Arg	Val	Leu	Ile	
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Tyr	Ser	Gln	Phe	Gln	His	Met	Leu	Asp	Leu	Leu	Glu	Asp	Tyr	Leu	Ser	
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Phe	Cys	Phe	Leu	Leu	Ser	Thr	Arg	Ala	Gly	Gly	Leu	Gly	Ile	Asn	Leu	
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